

C1
COW+ 3. (Amended) The method of claim 1 wherein the mismatch repair gene is MutS.

4. (Amended) The method of claim 1 wherein the mismatch repair gene is MutL.

5. (Amended) The method of claim 1 wherein the mismatch repair gene is MutY.

Sub D4 12. (Amended) The method of claim 3 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.

13. (Amended) The method of claim 4 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.

C2 14. (Amended) The method of claim 6 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.

15. (Amended) The method of claim 7 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.

Sub D4 16. (Amended) The method of claim 4 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation at codon 134.

17. (Amended) The method of claim 6 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation at codon 134.

Sub D4 18. (Amended) A homogeneous composition of cultured, hypermutable bacteria which comprise a polynucleotide encoding a form of a mismatch repair protein under the control of an inducible transcription regulatory sequence, wherein said polynucleotide exerts a dominant negative effect when expressed in said bacteria.

C3 D4 26. (Twice Amended) The homogeneous composition of claim 20 wherein the bacteria express a protein which consists of the first 133 amino acids of PMS2.

C4 31. (Amended) The homogeneous composition of claim 23 comprising a protein which consists of a eukaryotic MutS protein.